

FIG. 1

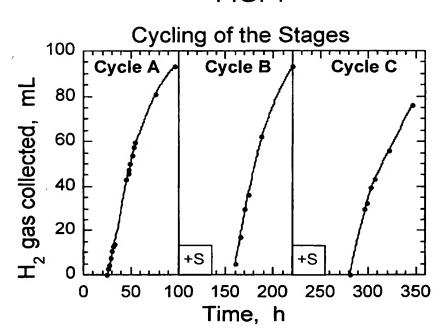


FIG. 2

Chlamydomonas reinhardtii chloroplast Sulfate Permease (SulP) gene structure



FIG. 3

reinhardtii chloroplast Sulfate Permease (SulP) amino acid sequence

MERVCSHQLASSRGRPCIAGVQRSPIRLGTSSVAHVQVSPAGLGRYQRQRLQVVASAAAA
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LPFALPTSVAGLTLATVYGDEFFIGQFLQAQGVQVVFTRLGVVIAMIFVSFPFVVRTMQP
VMQEIQKEMEEAAWSLGASQWRTFTDVVLPPLLPALLTGTALAFSRALGEFGSIVIVSSN
FAFKDLIAPVLIFQCLEQYDYVGATVIGTVLLLISLVMMLAVNQLQKLARK*(SEQ ID NO:1)

FIG. 4A

Coding sequence of CrcpSulP

5' UTR:173 bp, Exon1: 124 bp, intronI: 77 bp, Exon2: 78 bp,

intronII: 279 bp Exon3: 620 bp, intronIII: 834 bp,

Exon4: 87 bp, intronIV: 699 bp, Exon5: 327 bp, 3'UTR: 575 bp

Total length: 3873 bp

```
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gtaagccacc agacactacc aagtagagta atccatttgt ataggtacag aatatggagc 180
gagtttgcag ccatcagctt gcctcgtcgc gagggaggcc atgcatcgct ggggtgcagc 240
ggtegeceat eegactaggg aetteaageg ttgeteatgt geaggtetet eeggeaggta 300
agcaccgcgc teggeggegt gtacacatgg ggccgtcagg ccaactgcgt ttgttggcta 360
tgcaaccgaa acaggeettg ggagatatca acggcaaaga ctgcaagtcg tggcgtctgc 420
agetgeggea geggettteg acceteetgg aggtgegtgg egtgaggget geaegggtge 480
gggttggcct ggaaaccaag cctcgccacq actacctgca acaqcattqc ccqcatctcc 540
agececteae cetegagtge etecegaaga eetetateee etgegeatea ttggtteggg 600
ggcqccgcct gcgggccttg ggcgctggct acgctgaccg cacggcacga cttggcacgg 660
cetggegegg cetgagegge ecceecete etgatggeec eaegetttge egeceaegee 720
geteceegea ggtgteteeg eegggttete geageegeaa eageagetge cacaacagea 780
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cccgcagttg gaggatgctc cacgcgcttc agcttgccat gtctggggtc tgggtctgga 2040
cgcaatcagc gtgtgagggt ccaactctat atggaattat ggatacettc caactaccag 2100
cacqtagget geeggaacge ggetgaageg getggeetge eeeetcatee tetegtteee 2160
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FIG. 4B

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				gcgggttggg		
				gcagcctggc		
				gaaggggaag		
gcgagcaaag	ggggtatggg	aaccggcggt	tggggctggg	agcgacggga	gcagggaggg	2520
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atggtcgctg	ggcgcctcgc	agtggcgcac	cttcacagac	gtggtgctgc	cgccgctgct	3060
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				gggattgatt		
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tgcaagctca	ggcagtcgca	tgcccgtacc	ctgcttctgg	tccagtgtgg	agacaagact	3840
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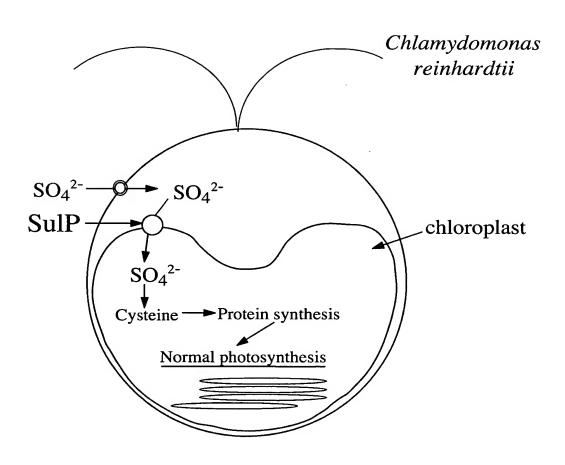
FIG. 5

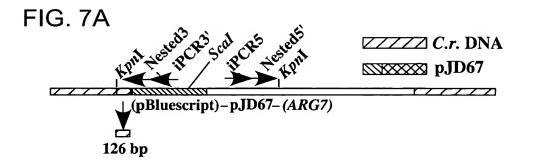
Full length cDNA sequence of CrcpSulP: 1984 bp

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ggtegeceat cegaetaggg actteaageg ttgeteatgt geaggtetet ceggeaggee 300
ttgggagata tcaacggcaa agactgcaag tcgtggcgtc tgcagctgcg gcagcggctt 360
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tcaacqtctt catcqcqcqc qccaccqaqc cqqtqqcqat qcacqcctac tacqtcacct 780
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                                                                1984
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(SEQ ID NO: 3)

FIG. 6





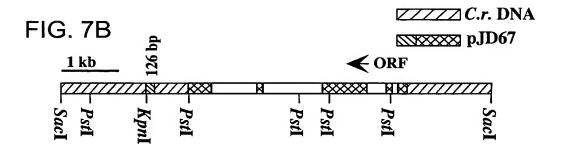


FIG. 8A

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Nephroșelmis Mesostigma Chlamydomonas Chlorella Syn.PCC7942 Marchantia	Nephroselmis Mesostigma Chlamydomonas Chlorella Syn. PCC7942 Marchantia Bacillus	Nephroselmis Mesostigma Chlamydomonas Chlorella Syn.PCC7942 Marchantia Bacillus	Nephroselmis Mesostigma Chlamydomonas Chlorella Syn. PCC7942 Marchantia Bacillus

FIG. 8A

```
112111
67465050
64444
                                                                                                 222222
242222
24222
2504444
224222
8046787
4046880
                                                                                                                                                                                        IPFODLIAPVLIFORLEQYDYSGATVIGTVVLLISLTLLLAINWIOASNRKFLG-
IPFROLTAPVLIFOKLEQYDYTGATVIGTVILSISLFILVGINIIOSLNOMYSK-
FAFKDLIAPVLIFOCLEQYDYVGATVIGTVLLLISLVMMLAVNOLOKLARK---
LPFKDLVASVLIYOSLEQYDYLGASVIGAVVLLIALFTLLLINAFOIMKFRV---
IPFNDLVIPFELIAPVLIFFRLEQYDYAGATVIGSVLLIFSLVIINALONWSSRYNG--
IPPNCDLVISVLLFOKLEQYDYKSATIIASFVLIIFSTVALFFINKIOLWKKTFHK-
LPMQTEITPLLIMTKLEQFDYAGATALAAVMLIISFFMLLFFINKIOLWKKTFHK-
LPMQTEITPLLIMTKLEQFDXAGATALAAVMLIISFFMLLFINILQWWSQRRQLS
                                                                                              Nephroselmis
Mesostigma
Chlamydomonas
Chlorella
Syn. PCC7942
Marchantia
 Nephroselmis
Mesostigma
Chlamydomonas
Chlorella
Syn. PCC7942
Marchantia
Bacillus
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Chlamydomonas
Chlorella
Syn.PCC7942
Marchantia
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FIG. 8B

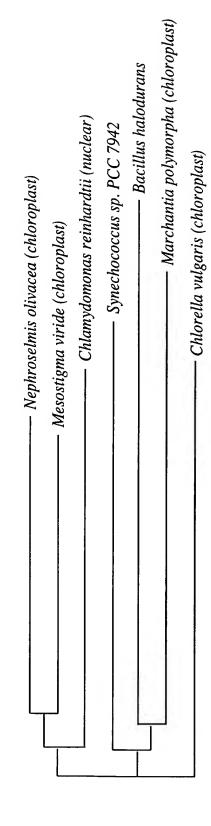


FIG. 9

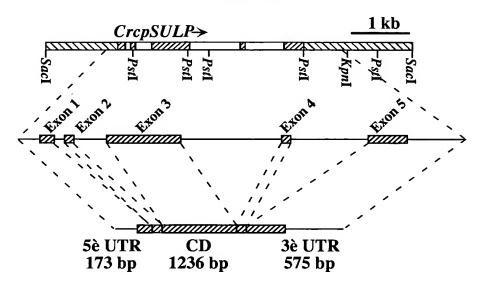
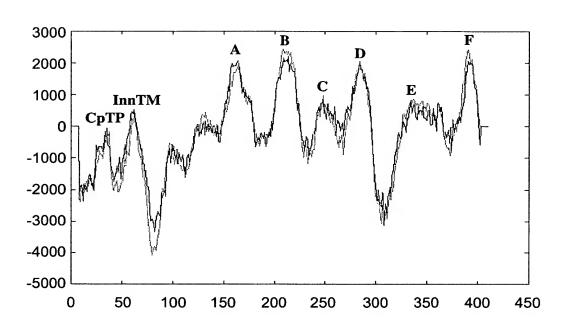
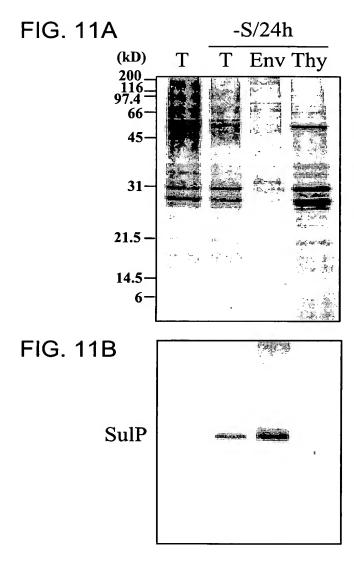
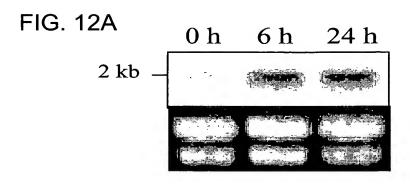
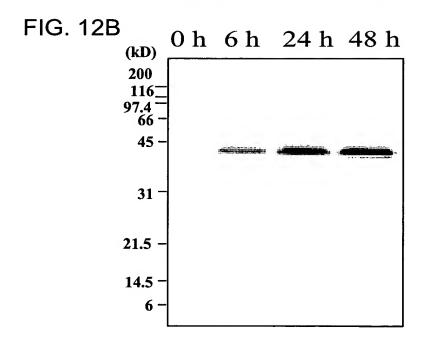


FIG. 10









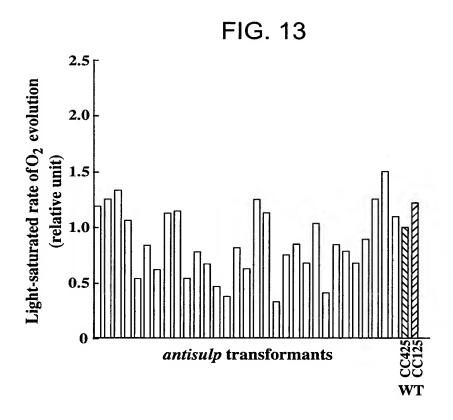


FIG. 14A

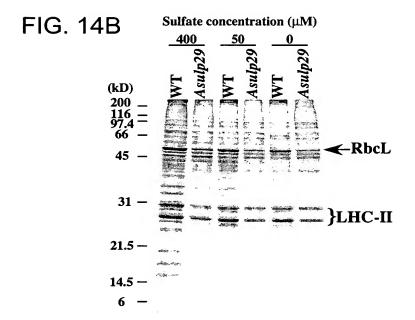
Sulfate concentration (μM)

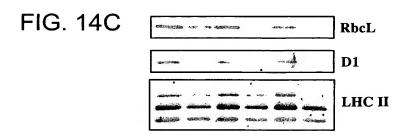
400 50 0

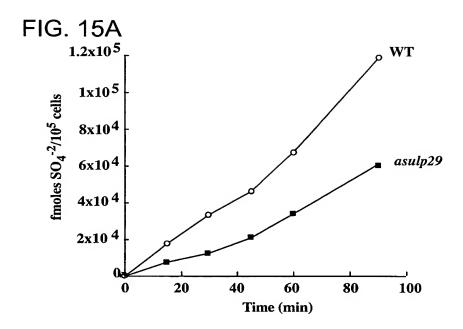
67d μ μ μ ss

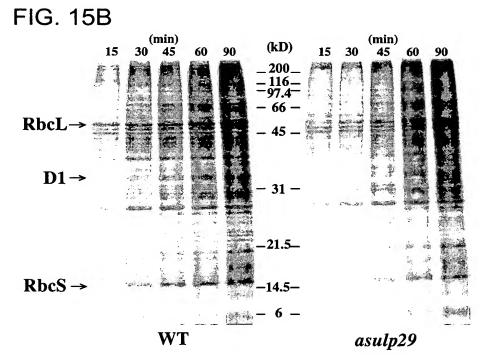
L μ ss μ ss μ ss

CrcpSulP









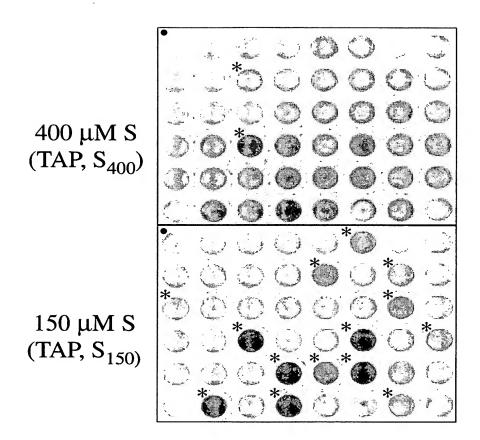
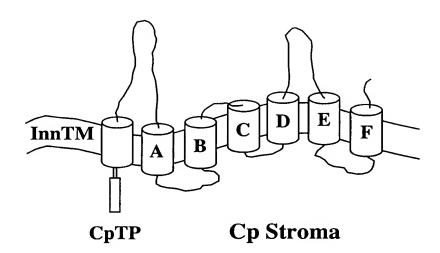
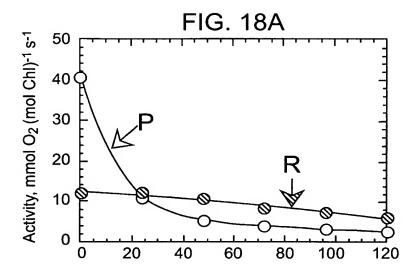


FIG. 16

FIG. 17





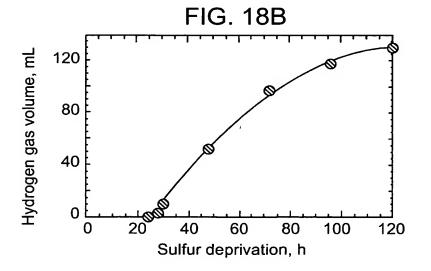


FIG. 19

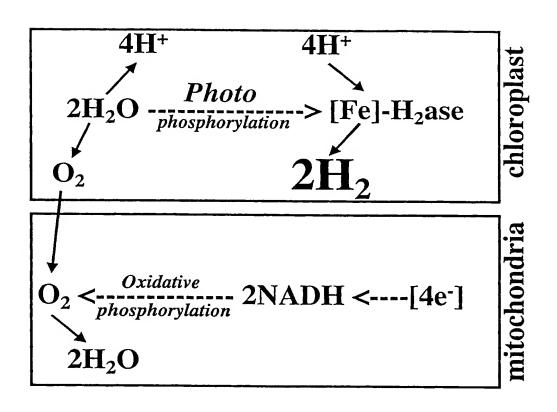
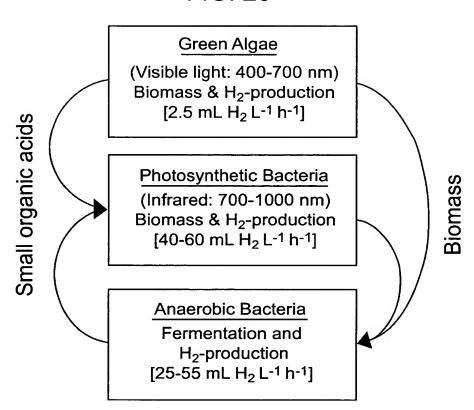


FIG. 20



CATTCAATTTGCAGCGTTCCTAAAATGGCAAGCACACGCTGCTCCAGCCCGCGCTTGGTCTGCCCTCGCGGGTAGGG GACTCATCATCAGTTATAGAGAGCACGCTAGGGCGGCAAACATCGGTTGCCGGGAGACCATGGCTTGCACCCCGGCCT GCGCCTCAA CAAAGCCGAGGCGACCTACTGGTCTCCAAATCGGGGGCAGCAGGAGGCATGGGCGCCCATGGAGGGGGC TTAGGGGAACCGGTCGATAATTGGATCAAGAAGCTACTCGTTGGTGTCGCGGCGGCGTACATCGGCTTGGTCGTGCTG GTGCCCTTCCTGAATGTCTTCGTCCAGGCGTTCGCCAAGGGCATCATTCCCTTCCTGGAGCACTGCGCGGACCCGGAC TTTCTGCACGCACTCAAGATGACGCTGATGCTGGCGTTCGTGACGGTGCCGCTCAACACGGTGTTTGGCACGGTGGCC GCGATCAACCTCACGCGCAACGAGTTCCCCGGCAAGGTGTTCCTGATGTCGCTGCTGGACCTGCCCTTCTCCATCTCG $\tt CCCGTGGTGACTGCTCACGCTGCTGTACGGCCGCACCGGCTGGTTCGCGGCGCTGCTGCGGGGAGACCGGC$ ATCAACGTGGTGTTCGCATTCACGGGCATGGCCCTGGCCACCATGTTTGTGACGCTGCCGTTCGTGGTGCGCGAGCTG ATCCCCATCCTGGAGAACATGGACCTGTCGCAGGAGGAGGCGGCGAGAACGCTGGGGGGCCCAACGACTGGCAGGTGTTC TGGAACGTGACGCTGCCCAACATCCGCTGGGGCCTGCTGTACGGCGTGATCCTGTGCAACGCCCGAGCCATGGGCGAG AAGGAGTACAACACGGAGGCGCGTTCGCGGCGGCTGTGCTGCTGAGCGCGCTGGCGCTGGGCACCCTGTGGATCAAG GACAAGGTGGAGGAGGCGGCGGCGGGGGAGAGCCGCAAG<u>TAG</u>AGAGGAGCAGCGGCGGCGGCGGCGGCGGCAGTGGC GGAGGCAGGCGCCGACGCGAGGGGAGGGCGTGGTGGTGGGCTTGCGTGGGTGCTTGGTCCGTGGCCAGGGTGCCTGGC AGTGCCGCAGTGACCAGCGGGTAATGGTAAGGGAGCTGACACGTGTGGCGTTCTGTTGCTGGTCGCCGCATGCTTAAC GCAGCGGGAGCAGCTTCTCTGTCTGATGTCTAACGGGGGCGTTGTATGCTGATAATAGACGGAGGGCGAAGGGAGCAG GTGTTGACGGTACAGTTATGCCGTGCCCCGTTTTACAAGCGGGATAGAGGCACACTCCACGTAGTATGCATTGAGCCC AGTAGACTCTGGTCAGAAGGCCGGTAAATTTACATGTGTCGTGGTGAACCCTGTAAGTCATGGCCCAAG (SEO ID NO: 04)

GTACTTCAATTGTCAGAATGGCGTCGCTGCTCGCTCAAACAACATCGCGCCTTGGCGCTCGCCCAGCTGCGCAA GCTGGCCCTGTCGCCCAAATGGCACCGATGGCAAGCCGAGTGCAGCCGGCGATGCCTAGCGCGCTGCTCCCACT GAGATTCGTCGCAACAGTCCTCCAATGGGGCAGGAGAAGTGTCCATGTCCATATCATCCATGGACGAGGTTGGA CCCTCTTATGAGGGAATCATTACAGACGCGCCTACACGACCAACGGGGCTTTATGTGCGGGTGCGCAACATGGT GAAGCACTTCAGCACCGCCAAAGGCCTGTTCAGGGCGGTGGACGGCGTGGACGTGGACATCGAGCCCAGCTCCA GTTCCAGAGCTATGCGCTGTTCAACCACAAGACAGTTGCGGAGAACATCAAGTTTGGACTGGAGGTGCGCAAGC TCAACATCGACCACGACAAGCGCGTGGCGGAGCTGCTGGCGCTGGTGCAGCTCACCGGCCTGGGCGACCGCTAC CCGCGCCAACTGTCGGGCGGCCAGCGGCAGCGTGTGGCGCTGGCGCCCCTGGCCTCCAACCCGCGGCTGCT GCTGCTGGACGAGCCCTTTGGCGCGCTGGACGCGGTGGTGCGCAAGCAGCTGCGCACGGGGCTGCGCGAGATCG TGCGCAGCGTGGCCTGACCATCATTGTGACGCACGACCAGGAGGAGGCGTTCGACCTGGCGGACAAGGTG GTGGTGTTCAACAGGGGCCTGGTGGAGCAGCAGGGCAGCCCCACCGAGATCATCAAGCGGCCGCGCACGCCCTT CATTATGAAGTTCGTGGGCGAGACCAACGTGGTGCCGGCCACGTCGCTGCTGGCCAAGCGCATGCGCTTCAACA CCTCCAAGACCAGCGTCATGTTCCGGCCGCACGACATTAAGCTGTTCAAGACGGTGCCGCCGGAGAGCGGCGAG GGCGCGCTGACCACGGTGGGCGCCAACGTGGCGGACAAAGCCAACCTGGGCTGGGTGGTCAAGTACACGCTGCG CTTCGATGACGACGTGGAGTGCGAGCTGCAGCTCAGCCGCGACCAGGACGAGCGCGAGTACAACCTGGTGGTGG GCAGCCGCGTGTTCGTGCACGTGCCGCACCGCACCATGATGGGCTTCAACGCCAGCGACGTGGACAGCACGCCC ATCGTGTAATGTGCGGGGTTGGCCGCTGTGGCCAGCGATTGTTGCAATGCAGTCCAGCGTGCTCTTGGTTTGGT TCCAGTGACACCCATCCAGGGCACAGGTCCCTGAGCAGCGGGTGTTGGTGATGGGTTTGGAGCAGTTGTACCCGA TTCTCGCATGCAAGGGGCGGGGGCCCCACGGGGTGGGAGAGCGGAATGGCGGTGAGGTGGGCTACTGCATGCG TTGGGGGTGGAGGCCGTGCAGACTGGTTGGGATACTGACAGATCAATGAGCGGCGTCTGCTCCATGGGTCAGTA CGTCTGCGGGCGCTGTCGGAGACGGCGATGTACATGAAGCTGGACCTGGGCCTGTCTCACAAATATCCCTTAT GTTAATAGTAGGATGTCGCAATCGTGCCTTGGAGCCCACCTGATGTGTGTCTCACAGGTGGCAGTAGTTTGGCC TGAAACCATGCATCATGCGTGCTATCAGGAGATGCAGACGGCGGATTGCTGCCAAAATGTTCTGTTGTTGGTGT GCAGACTTGGTGGCGAAGGGGCCAGGCGC CCAGGGGTATGCTGCCTGCCAAGGAGCTGCTGCCGCCACGAGTGA CCAGCGAAACTTGTAAATTGAATATTGTATCCT (SEQ ID NO: 05)

GGGCAGCGTATAAGTAATGTCGTTCTTGGCTCCCAGCTTAGGCGTCGCGCGGGGGATTCTGGAGCCGGCGAGTGC AGCGAGGCCGCCTGCGCACGCGGCCGGTCACGCACCCGTTCTAACAAGCGATAGGACTGGTGGACCTGCCGCTAA GCAAGGCGACCCCAGCGCTCGCAGCACCAGCAAGCGCCAGGCAGCAGCAGCAGTCGCAGTCGCGGTCGCT CCAATCACACCTCATCACCGCGGCCACGCTGCTGCCAGCCCTGCCGCCTCCCGGCGGCGAACGGCGACGG CGATGGCGGCGAAGCTGCGGGGCCGCAGCCGCTCGCGGACGTCAGCCGCCGGAGGTTGTGCTGACGCT GGGCGTGGATGTGCGCTTCCGCCTCACCTTCGCCGCCAGTGGCGTGCAGGCCCGCGCGTGATCGATGGCCTGCC CGCCGACATCGTGGCCCTGGCGCTCCTGGACCTGGACAAGATCGTGTCGGCGGGGCTGATCCGGCCCGACTG GCGCAGCGCCTACCCGGCAGCCAGCGTGGTGTGCGAGACCACCGTGGCGTTCGTGGTGCGCCAGGGCAACCCCAA GAACATCCGCACCTGGGAGGACCTCACGCGGGCGGGTGTGGAGGTGCTGGCCAACCCCAAGACCCGCGGAGT GGCCAGGTGGATCTTCCTGGCCCTGTGGGGCGCCAAGATGAAGAAGGGCAACGCCGCCGCGCTGGCGTATGTGCA GCGCGTGTTCGAGAACGTGGTGCTGCAGCCGCGTGATGCGCGCGAGGCGTCGGACGTGTTCTATAAGCAGAAGGT GGGCGACGTGCTGTTGACGTACGAGAACGAGGTGATCCTGACCAACGAGGTGTACGGCGACAAGGCGCTGCCGTA CCTGGTGCCCTCCTACAACATCCGCATCGAGTGCCCGCTGGCGCTGGTGGACAAGGTGGTGGATGCCCGCGGCCC GCAGGTGGACAAGGAGCTGGGCGGCTGGGCTGCGGCCCAGAAGAAGTTTTTCGACGCTGGCGCCATCCTTGACGA CATCCAGTCCGCCGTGGGCAAGCTGCGTGTGGAGCAGCGCAAGGCGGCGCAGGCGGCCAGGCGGTAGAGAGA $\tt CGCGGTACAAGTGCTCGGGTGCTCAGCAGGAGCTGCAGCAGGGGCAGCAAGAGGGGCCTTGACAGGAGGGAATGGT$ AGGCAAAGG CGGCAGGGGAGGCGGGATGGCGGGATGAAGTGAGGTGTGCAAGCAGCGATGTGTGCCAAGGACGG TGTCGGCGATGTACATGATAACATGAGGAGACAGGAGCATCTCCTGGCAGGAGGCGGCAACCGTGGAGTGTCTGA AAGGAGAACTTGATTGCTCAGTGTGGGACAGATAACGGAGGGCGGGGTGTGGGGCCTTATCGGTGTGCT TCTATGGGGAGGCCTGACTGCATTGGGGGCGACGTAGTGTGATGGCCGCTACACGCTTGCTCGGAACTGACATAA ACAGGCGTTCAGGCCATGGCTGCATGAGGCTTGATGTCGTATCGCGGACTGTC (SEQ ID NO: 06)

MASTTLLQPALGLPSRVGPRSPLSLPKIPRVCTHTSAPSTSKYCDSSSVIESTLGRQTSV
AGRPWLAPRPAPQQSRGDLLVSKSGAAGGMGAHGGGLGEPVDNWIKKLLVGVAAAYIGLV
VLVPFLNVFVQAFAKGIIPFLEHCADPDFLHALKMTLMLAFVTVPLNTVFGTVAAINLTR
NEFPGKVFLMSLLDLPFSISPVVTGLMLTLLYGRTGWFAALLRETGINVVFAFTGMALAT
MFVTLPFVVRELIPILENMDLSQEEAARTLGANDWQVFWNVTLPNIRWGLLYGVILCNAR
AMGEFGAVSVISGNIIGRTQTLTLFVESAYKEYNTEAAFAAAVLLSALALGTLWIKDKVE
EAAAAESRK* (SEQ ID NO: 07)

MASLLAQTTSRLGARPAAQAGPVAQMAPMASRVQPAMPSALLPLHARATTTSVAC
RAASIDKPVVYTPRDSSQQSSNGAGEVSMSISSMDEVGPSYEGIITDAPTRPTGL
YVRVRNMVKHFSTAKGLFRAVDGVDVDIEPSSIVALLGPSGSGKTTLLRLIAGLE
QPTGGNIYFDDTDATNLSVQDRQIGFVFQSYALFNHKTVAENIKFGLEVRKLNID
HDKRVAELLALVQLTGLGDRYPRQLSGGQRQRVALARALASNPRLLLLDEPFGAL
DAVVRKQLRTGLREIVRSVGVTTIIVTHDQEEAFDLADKVVVFNRGLVEQQGSPT
EIIKRPRTPFIMKFVGETNVVPATSLLAKRMRFNTSKTSVMFRPHDIKLFKTVPP
ESGEGALTTVGANVADKANLGWVVKYTLRFDDDVECELQLSRDQDEREYNLVXGS
RVFVHVPHRTMMGFNASDVDSTPIV* (SEQ ID NO: 08)

MSFLAPSLGVARGILEPASAARPPAHAAGHAPVLTSDRTGGPAANHDRPAGAPSPH AASLTPSSSGQASQQGDPQRSQHQQAQRQDQQQSQSRSLQSHLITAATLLPALPPPP PGGNGDGDGGEAAGPQPLADVAAQPPEVVLTLASFAVTKLAYVRVTRAFREWYE RTKGVDVRFRLTFAASGVQARAVIDGLPADIVALALPLDLDKIVSAGLIRPDWRSA YPAASVVCETTVAFVVRQGNPKNIRTWEDLTRAGVEVVLANPKTAGVARWIFLAL WGAKMKKGNAAALAYVQRVFENVVVQPRDAREASDVFYKQKVGDVLLTYENEV ILTNEVYGDKALPYLVPSYNIRIECPLALVDKVVDARGPEVREAASEFCRFLFTPAA QHEFARLGFRVNPRTCKEVAAQQTGLPPANLWQVDKELGGWAAAQKKFFDAGAI LDDIQSAVGKLRVEQRKAAQAAARR* (SEQ ID NO: 09)

FIG. 27

Chloroplast Sulfate Transport System

